Genome Gene Best Homologs

Find corresponding genes between a reference and a set of up to 50 query isolate genomes. Please note that this tool is for isolate genomes only. For metagenome analysis, please use **Phylogenetic Distribution** option under **Compare Genomes** menu.

In order to use this function, a user first selects a reference isolate genome (e.g., *Acidianus hospitalis*) and then selects between 1 and 50 query genomes (e.g., *Aciduliprofundum boonei T469* and *Aciduliprofundum sp. MAR08-339*) for comparison. The user can also specify that the genes should not have homologs in a set of genomes to be excluded (e.g., adding *Caldisphaera lagunensis DSM 15908* to the **Excluded Genomes** list). The default percent identity is set to 60% and the value can be changed in the **Percent Identity** drop down list (see Figure 1(i)).

After the user clicks the **Submit** button, the **Genome Gene Best Homologs** result page (Figure 1(ii)) shows all genes in the reference genomes that have homolog genes with at least 60% identity in the reference genomes, and do not have homologs in the **Excluded Genomes**.

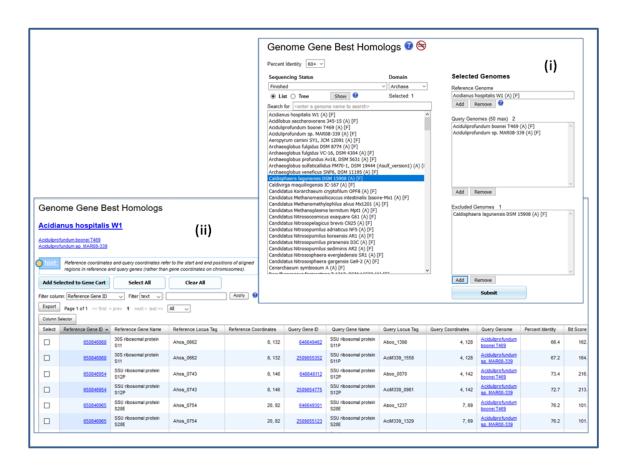


Figure 1. Genome Gene Best Homologs.

Users can select genes in the result page to be added to the Gene Cart for further analysis.

Reference genome and genes, as well as query genome(s) and genes can be examined following the corresponding hyperlinks in the result page.